Class 7: Machine learning 1

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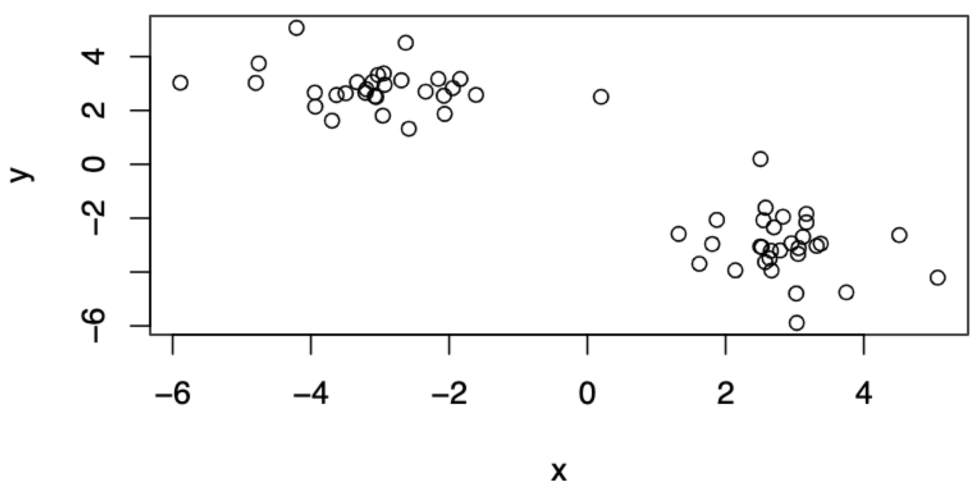
K-means Clustering

```
tmp <- c(rnorm(30,-3),rnorm(30,3))
x <- cbind(x=tmp,y=rev(tmp))
plot(x)
```




```
km <- kmeans(x,centers=4,nstart=20)
km
```

```
K-means clustering with 4 clusters of sizes 20, 20, 10, 10

Cluster means:
          x         y
1 -3.577610  3.017807
```

```
2  3.017807 -3.577610
3  2.449544 -1.937827
4 -1.937827  2.449544

Clustering vector:
 [1] 1 1 1 4 4 4 1 1 1 1 1 1 4 1 1 1 1 1 4 4 1 1 4 1 4 1 1 4 4 1 2 3 3 2 2 3 2 3
[39] 2 2 3 3 2 2 2 2 2 3 2 2 2 2 2 2 3 3 3 2 2 2

Within cluster sum of squares by cluster:
[1] 23.87626 23.87626  9.66856  9.66856
 (between_SS / total_SS =  94.1 %)

Available components:

[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
[6] "betweenss"    "size"         "iter"         "ifault"
```

```r
km$size
```

```
[1] 20 20 10 10
```

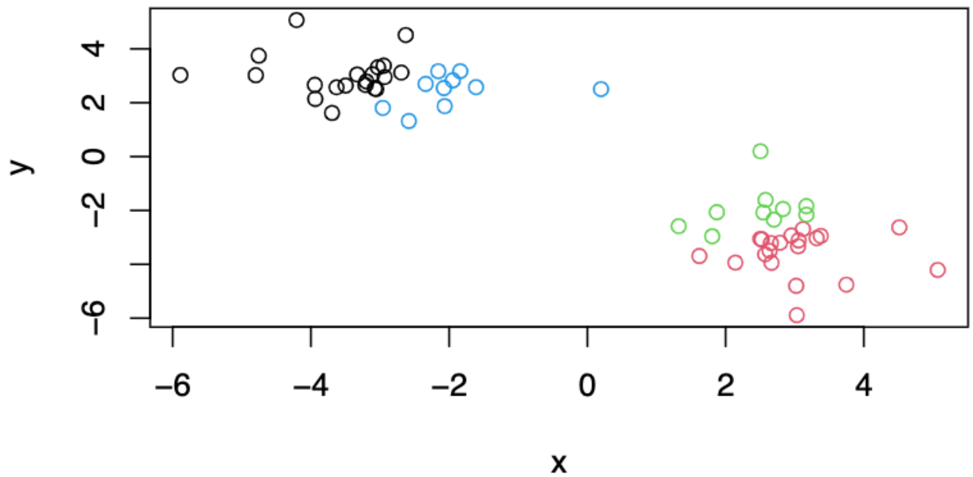
```r
km$cluster
```

```
 [1] 1 1 1 4 4 4 1 1 1 1 1 1 4 1 1 1 1 1 4 4 1 1 4 1 4 1 1 4 4 1 2 3 3 2 2 3 2 3
[39] 2 2 3 3 2 2 2 2 2 3 2 2 2 2 2 2 3 3 3 2 2 2
```

```r
km$centers
```

```
          x         y
1 -3.577610  3.017807
2  3.017807 -3.577610
3  2.449544 -1.937827
4 -1.937827  2.449544
```

```r
plot(x,col=km$cluster)
points(km$centers,col=km$clusters,pch=15,cex=2)
```



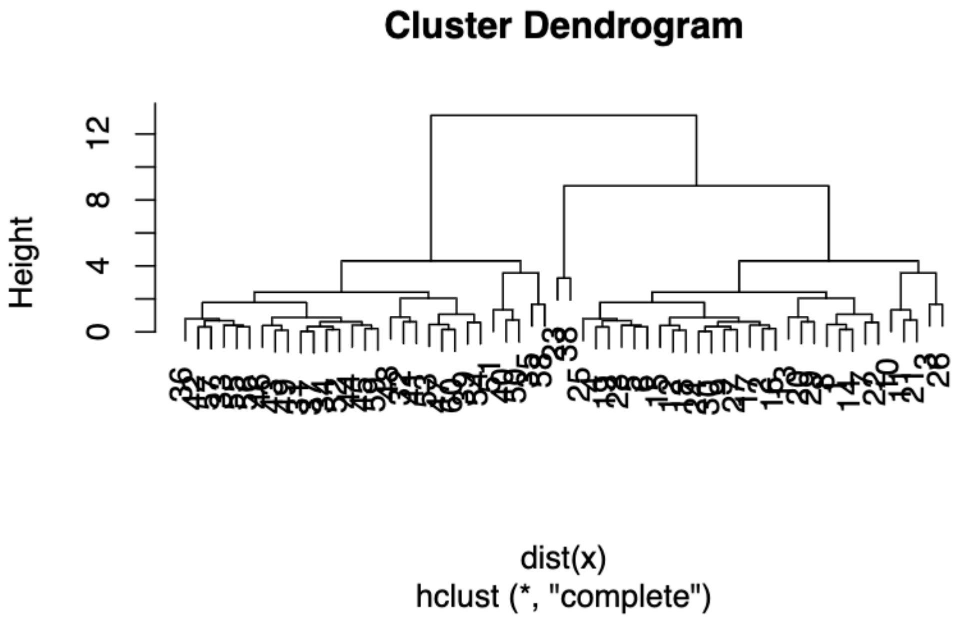

```
#rep(x,y) repeat membership x for y times
```

```
hc <- hclust(dist(x))
hc
```

```
Call:
hclust(d = dist(x))

Cluster method   : complete
Distance         : euclidean
Number of objects: 60
```

```
plot(hc)
```



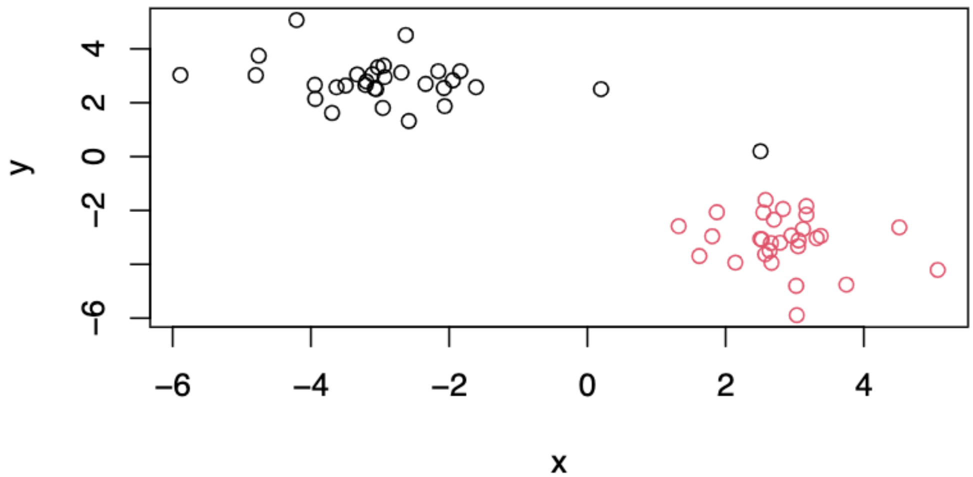

```r
cutree(hc,h=8)
```

```
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 3 3 3 3 3 3 3 2
[39] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
```

```r
grsp <- cutree(hc,k=2)
grsp
```

```
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 1
[39] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
```

```r
plot(x,col=grsp)
```



#Principal Component Analysis (PCA)

Q2. Which approach to solving the 'row-names problem' mentioned above do you prefer and why? Is one approach more robust than another under certain circumstances?

```
url <- "https://tinyurl.com/UK-foods"
x <- read.csv(url,row.names=1)
```

```
head(x)
```

```
               England Wales Scotland N.Ireland
Cheese             105   103      103        66
Carcass_meat       245   227      242       267
Other_meat         685   803      750       586
Fish               147   160      122        93
Fats_and_oils      193   235      184       209
Sugars             156   175      147       139
```

```
#rownames(x) <- x[,1]
#x <- x[,-1]
#x
```

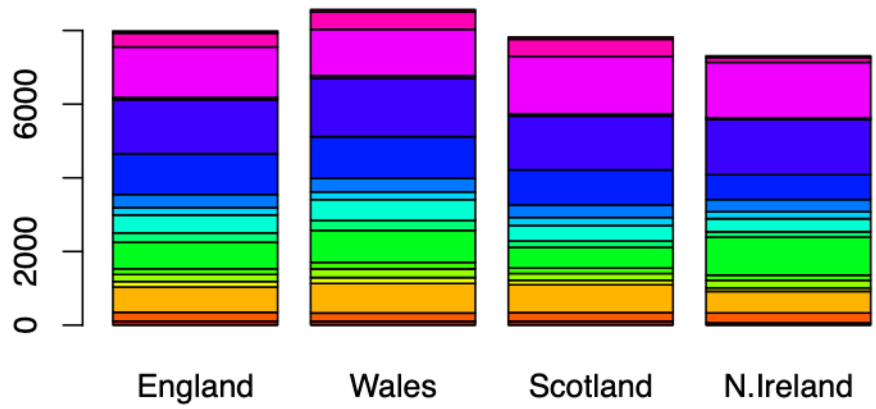
Q1. How many rows and columns are in your new data frame named x? What R functions could you use to answer this questions?

```
dim(x)
```

```
[1] 17  4
```

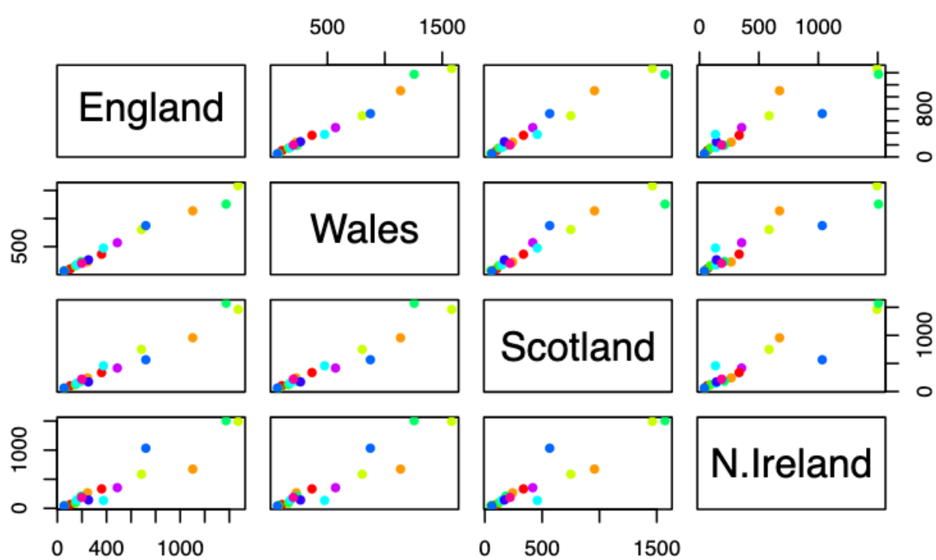
Q3: Changing what optional argument in the above barplot() function results in the following plot?

```r
barplot(as.matrix(x),col=rainbow(nrow(x)))
```



Q5: Generating all pairwise plots may help somewhat. Can you make sense of the following code and resulting figure? What does it mean if a given point lies on the diagonal for a given plot?

```r
pairs(x, col=rainbow(10), pch=16)
```



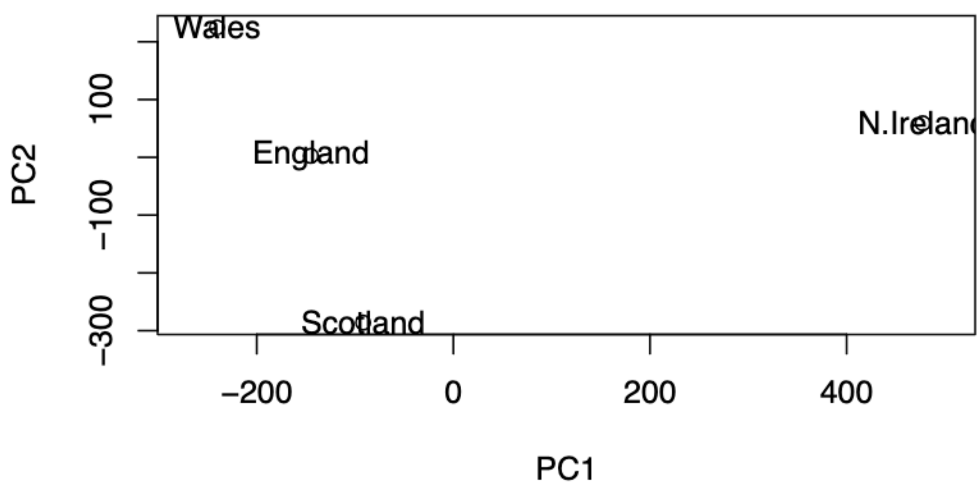
Q6. What is the main differences between N. Ireland and the other countries of the UK in terms of this data-set?

```
#prcomp expects the transpose of the data input
pca <- prcomp(t(x))
summary(pca)
```

```
Importance of components:
                            PC1      PC2      PC3       PC4
Standard deviation     324.1502 212.7478 73.87622 4.189e-14
Proportion of Variance   0.6744   0.2905  0.03503 0.000e+00
Cumulative Proportion    0.6744   0.9650  1.00000 1.000e+00
```

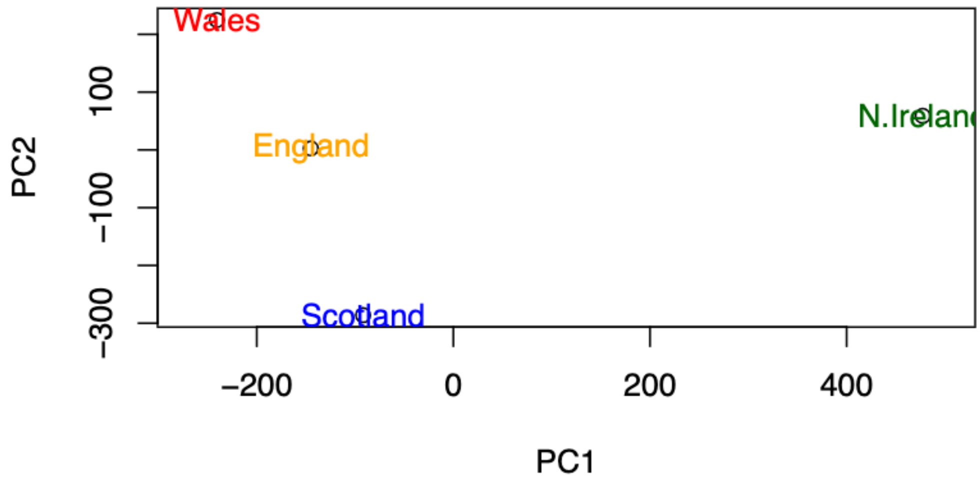
Q7. Complete the code below to generate a plot of PC1 vs PC2. The second line adds text labels over the data points.

```
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2", xlim=c(-270,500))
text(pca$x[,1], pca$x[,2], colnames(x))
```

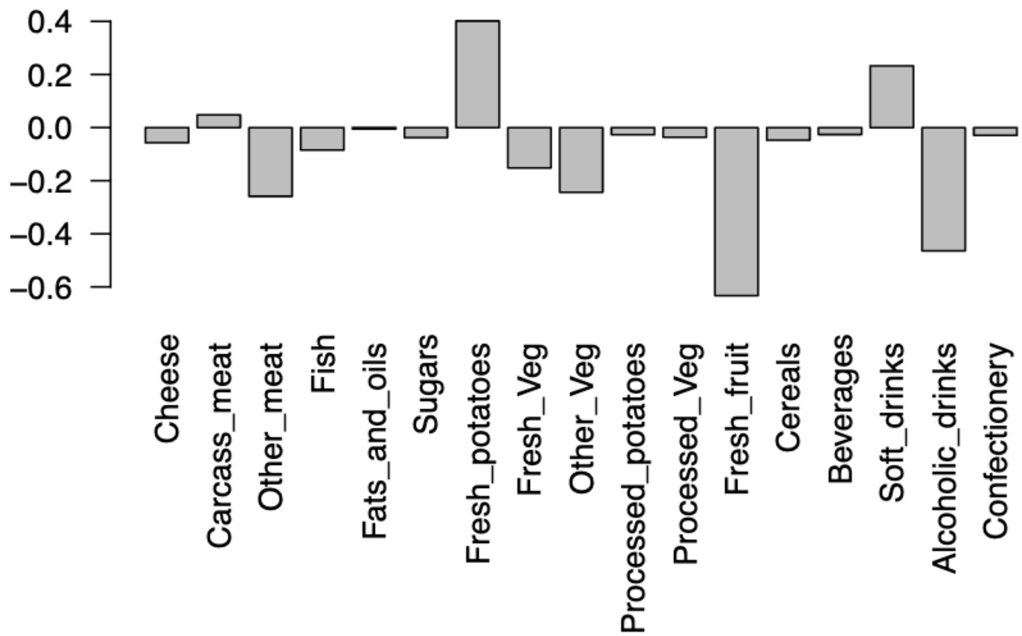


Q8. Customize your plot so that the colors of the country names match the colors in our UK and Ireland map and table at start of this document.

```
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2", xlim=c(-270,500))
text(pca$x[,1], pca$x[,2], colnames(x),col=c("orange","red", "blue","darkgreen"))
```

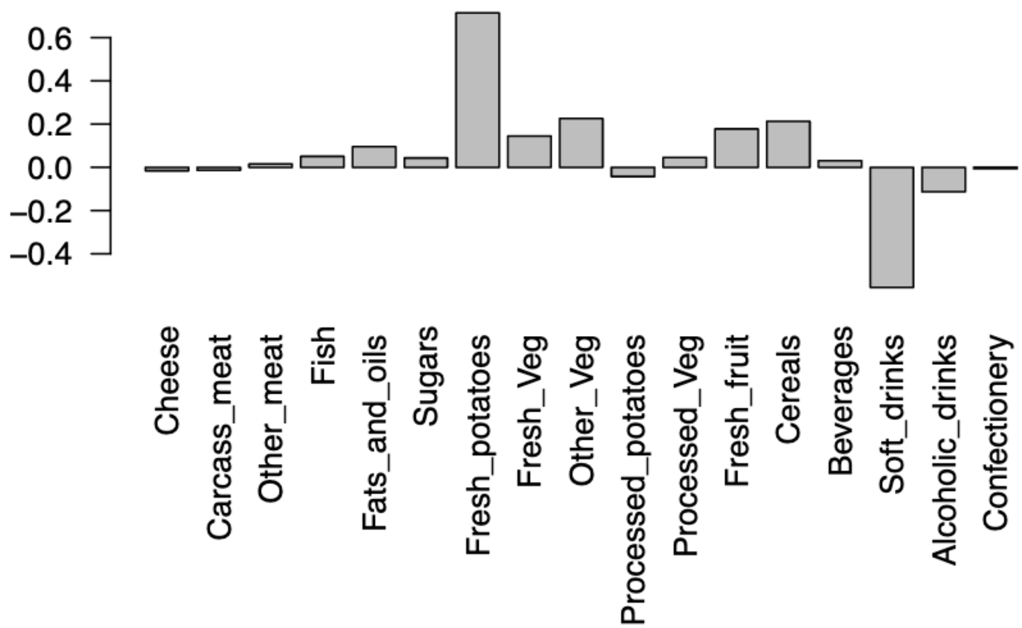



```r
par(mar=c(10, 3, 0.35, 0))
barplot(pca$rotation[,1], las=2)
```



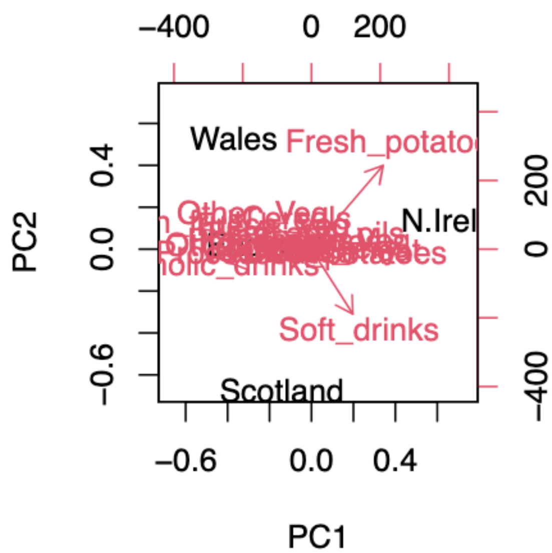
Q9: Generate a similar 'loadings plot' for PC2. What two food groups feature prominantely and what does PC2 maninly tell us about?

```r
par(mar=c(10, 3, 0.35, 0))
barplot(pca$rotation[,2], las=2)
```



0.6
0.4
0.2
0.0
−0.2
−0.4
Cheese
Carcass_meat
Other_meat
Fish
Fats_and_oils
Sugars
Fresh_potatoes
Fresh_Veg
Other_Veg
Processed_potatoes
Processed_Veg
Fresh_fruit
Cereals
Beverages
Soft_drinks
Alcoholic_drinks
Confectionery


```
biplot(pca)
```



−400
0
200
Wales
Fresh_potato
N.Irel
Soft_drinks
Scotland
PC2
PC1
−0.6
0.0
0.4